

L Number	Hits	Search Text	DB	Time stamp
-	368	(assay or screen or analysis) with (gene adj3 (function))	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/01/02 11:45
-	187	((assay or screen or analysis) with (gene adj3 (function))) and (antisense or ribozyme)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/01/02 11:45
-	163	((((assay or screen or analysis) with (gene adj3 (function))) and (antisense or ribozyme)) and (mammalian or drosophila or yeast or plant or (non adj2 bacterial))	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/01/02 11:46
-	0	(((((assay or screen or analysis) with (gene adj3 (function))) and (antisense or ribozyme)) and (mammalian or drosophila or yeast or plant or (non adj2 bacterial))) and (non adj2 bacterial)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/01/02 11:47
-	240	antisense and (non adj2 bacterial)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/01/02 11:47
-	163	(antisense and (non adj2 bacterial)) and function and phenotype	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/01/02 11:48
-	1	1999-405170.NRAN.	DERWENT DERWENT	2003/01/02 11:48

LAST RELOADED: Dec 20, 2002 (20021220/UP).

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(FILE 'HOME' ENTERED AT 10:52:45 ON 02 JAN 2003)

FILE 'CAPLUS, MEDLINE, BIOSIS' ENTERED AT 10:53:30 ON 02 JAN 2003

L1 28171 FILE CAPLUS
L2 30654 FILE MEDLINE
L3 25791 FILE BIOSIS
TOTAL FOR ALL FILES
L4 84616 S GENE AND FUNCTION AND (ALTERED OR ALTER OR CHANGE OR PHENOTYP
L5 620 FILE CAPLUS
L6 584 FILE MEDLINE
L7 438 FILE BIOSIS
TOTAL FOR ALL FILES
L8 1642 S L4 AND (ANTISENSE OR (ANTI(W)SENSE))
L9 0 FILE CAPLUS
L10 1 FILE MEDLINE
L11 0 FILE BIOSIS
TOTAL FOR ALL FILES
L12 1 S L8 AND GENE AND SEARCH AND TARGET
L13 1 FILE CAPLUS
L14 0 FILE MEDLINE
L15 0 FILE BIOSIS
TOTAL FOR ALL FILES
L16 1 S L8 AND (NON(W) (BACTERIAL OR BACTERIA))
L17 97 FILE CAPLUS
L18 4 FILE MEDLINE
L19 2 FILE BIOSIS
TOTAL FOR ALL FILES
L20 103 S EST AND ANTISENSE AND SCREEN?
L21 6 FILE CAPLUS
L22 1 FILE MEDLINE
L23 1 FILE BIOSIS
TOTAL FOR ALL FILES
L24 8 S L20 AND L8
L25 7 DUP REM L24 (1 DUPLICATE REMOVED)
L26 2 FILE CAPLUS
L27 0 FILE MEDLINE
L28 0 FILE BIOSIS
TOTAL FOR ALL FILES
L29 2 S L20 AND PY=<1997
L30 101 FILE CAPLUS
L31 36 FILE MEDLINE
L32 30 FILE BIOSIS
TOTAL FOR ALL FILES
L33 167 S ANTISENSE AND SCREEN AND GENE AND FUNCTION
L34 72 FILE CAPLUS
L35 18 FILE MEDLINE
L36 11 FILE BIOSIS
TOTAL FOR ALL FILES
L37 101 S L33 AND (MAMMALIAN OR HUMAN OR CHO)
L38 101 FOCUS L37 1-
L39 72 S L38
L40 4 FILE CAPLUS
L41 18 S L38
L42 0 FILE MEDLINE
L43 11 S L38
L44 0 FILE BIOSIS
TOTAL FOR ALL FILES

L45 4 S L38 AND ANTISENSE AND RIBOZYME
 L46 2820 FILE CAPLUS
 L47 388 FILE MEDLINE
 L48 488 FILE BIOSIS
 TOTAL FOR ALL FILES
 L49 3696 S GENE(W) DISCOVERY
 L50 29 FILE CAPLUS
 L51 0 FILE MEDLINE
 L52 1 FILE BIOSIS
 TOTAL FOR ALL FILES
 L53 30 S L49 AND ANTISENSE AND (PHENOTYPE OR FUNCTION)
 L54 30 FOCUS L53 1-

FILE 'USPATFULL, PCTFULL, WPIDS' ENTERED AT 11:11:15 ON 02 JAN 2003

L55 12448 FILE USPATFULL
 L56 13331 FILE PCTFULL
 L57 339 FILE WPIDS
 TOTAL FOR ALL FILES
 L58 26118 S ANTISENSE AND GENE AND (DISCOVERY OR SCREEN) AND (FUNCTION OR
 L59 5040 FILE USPATFULL
 L60 6515 FILE PCTFULL
 L61 110 FILE WPIDS
 TOTAL FOR ALL FILES
 L62 11665 S L58 AND RIBOZYME
 L63 4868 FILE USPATFULL
 L64 6352 FILE PCTFULL
 L65 98 FILE WPIDS
 TOTAL FOR ALL FILES
 L66 11318 S L62 AND (HUMAN OR MAMMALIAN)
 L67 3623 FILE USPATFULL
 L68 4710 FILE PCTFULL
 L69 0 FILE WPIDS
 TOTAL FOR ALL FILES
 L70 8333 S L66 AND (SITE AND DIRECTED AND MUTAGENESIS)
 L71 3466 FILE USPATFULL
 L72 4533 FILE PCTFULL
 L73 0 FILE WPIDS
 TOTAL FOR ALL FILES
 L74 7999 S L70 AND INHIBIT
 L75 3457 FILE USPATFULL
 L76 4522 FILE PCTFULL
 L77 0 FILE WPIDS
 TOTAL FOR ALL FILES
 L78 7979 S L74 AND EXPRESSION AND VECTOR
 L79 31603 FILE USPATFULL
 L80 29235 FILE PCTFULL
 L81 6331 FILE WPIDS
 TOTAL FOR ALL FILES
 L82 67169 S L78 AND PHENOTYPE AND TRANSCRIPTION OR MRNA
 L83 2465 FILE USPATFULL
 L84 3222 FILE PCTFULL
 L85 0 FILE WPIDS
 TOTAL FOR ALL FILES
 L86 5687 S L78 AND PHENOTYPE AND TRANSCRIPTION AND MRNA
 L87 52 FILE USPATFULL
 L88 158 FILE PCTFULL
 L89 0 FILE WPIDS
 TOTAL FOR ALL FILES
 L90 210 S L86 AND PY=<1997
 L91 52 FILE USPATFULL
 L92 158 FILE PCTFULL
 L93 0 FILE WPIDS

TOTAL FOR ALL FILES
L94 210 S L90 AND ANTISENSE AND RIBOZYME
L95 4 FILE USPATFULL
L96 13 FILE PCTFULL
L97 0 FILE WPIDS

TOTAL FOR ALL FILES
L98 17 S L94 AND "ALTERED FUNCTION"
L99 5 FILE USPATFULL
L100 14 FILE PCTFULL
L101 0 FILE WPIDS

TOTAL FOR ALL FILES
L102 19 S L94 AND (ALTERED (3W) FUNCTION)
L103 1 FILE USPATFULL
L104 1 FILE PCTFULL
L105 0 FILE WPIDS

TOTAL FOR ALL FILES
L106 2 S L102 NOT L98

FILE 'CAPLUS, MEDLINE, BIOSIS' ENTERED AT 11:31:12 ON 02 JAN 2003

L107 0 FILE CAPLUS
L108 0 FILE MEDLINE
L109 0 FILE BIOSIS

TOTAL FOR ALL FILES
L110 0 S L94
L111 0 FILE CAPLUS
L112 0 FILE MEDLINE
L113 0 FILE BIOSIS

TOTAL FOR ALL FILES
L114 0 S L86
L115 0 FILE CAPLUS
L116 0 FILE MEDLINE
L117 0 FILE BIOSIS

TOTAL FOR ALL FILES
L118 0 S L78
L119 6 FILE CAPLUS
L120 4 FILE MEDLINE
L121 3 FILE BIOSIS

TOTAL FOR ALL FILES
L122 13 S KNOCK-OUT AND MUTAGENESIS AND ANTISENSE
L123 7 DUP REM L122 (6 DUPLICATES REMOVED)
L124 6 S L123
L125 3 FILE CAPLUS
L126 1 S L123
L127 1 FILE MEDLINE
L128 0 S L123
L129 0 FILE BIOSIS

TOTAL FOR ALL FILES
L130 4 S L123 AND FUNCTION AND GENE

FILE 'STNGUIDE' ENTERED AT 11:35:39 ON 02 JAN 2003

FILE 'CAPLUS, MEDLINE, BIOSIS' ENTERED AT 11:39:10 ON 02 JAN 2003

L131 81 FILE CAPLUS
L132 84 FILE MEDLINE
L133 65 FILE BIOSIS

TOTAL FOR ALL FILES
L134 230 S LOSS-OF-FUNCTION AND ANTISENSE
L135 4 FILE CAPLUS
L136 7 FILE MEDLINE
L137 3 FILE BIOSIS

TOTAL FOR ALL FILES
L138 14 S L134 AND (MAMMALIAN OR YEAST OR DROSOPHILA) AND PHENOTYPE

L139

9 DUP REM L138 (5 DUPLICATES REMOVED)

FILE 'STNGUIDE' ENTERED AT 11:41:28 ON 02 JAN 2003

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L139 ANSWER 6 OF 9 MEDLINE
 ACCESSION NUMBER: 97336333 MEDLINE
 DOCUMENT NUMBER: 97336333 PubMed ID: 9193109
 TITLE: Switching of gene expression: analysis of the factors that spatially and temporally regulate plant gene expression.
 AUTHOR: Meisel L; Lam E
 CORPORATE SOURCE: AgBio Tech Center, Rutgers, Cook College, New Brunswick, New Jersey 08903-0231, USA.
 SOURCE: GENETIC ENGINEERING, (1997) 19 183-99. Ref: 165
 Journal code: 7907340. ISSN: 0196-3716.
 PUB. COUNTRY: United States
 DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
 General Review; (REVIEW)
 (REVIEW, ACADEMIC)
 LANGUAGE: English
 FILE SEGMENT: Biotechnology
 ENTRY MONTH: 199707
 ENTRY DATE: Entered STN: 19970724
 Last Updated on STN: 19970724
 Entered Medline: 19970714

AB In this chapter, we have reviewed the present research and understanding of several families of transcription factors in plants. From this information, it appears there is good conservation between the types of transcription factors in plants and animals. However, there are several types of factors which have been isolated in plants that remain to be documented in animals (e.g., HD-Zip and GT). These as well as the presence of two types of TATA-binding proteins (TBPs) in plants suggest that although transcription in eukaryotes is highly conserved, fundamental differences may exist. Despite the differences, the modes of regulating transcription are well conserved. Figure 3 summarizes these modes of regulation. In recent years, the role of chromatin structure as well as subcellular localization have been the focus of a vast amount of research in mammals, *Drosophila* and yeast. However, very little research in these areas has been done in plants. Isolation of genes such as Curly leaf suggest a conservation of genes that influence the formation of heterochromatin-like structures. Whether or not this gene influences chromatin/heterochromatin structure in plants, however, remains to be tested. The study of nuclear localization of factors such as COP1 and KN1 is now leading to models for regulating nuclear transport as well as intercellular transport of transcription factors. Further study of the inter- and intracellular movement of these and other transcription factors may provide information on new modes of regulating transcription. In addition to understanding the role chromatin structure and subcellular localization of transcription factors may have on transcription initiation, the biological role of many plant transcription factors remains to be identified. Several approaches may be taken to understand the mechanisms by which transcription factors influence biochemical and physiological processes in the plant. These steps include 1) identification of the DNA-binding sites of the factors as well as the promoter regions which contain these sites. Presently, this approach is limiting in that not many non-coding regions have been sequenced and characterized in detail. Furthermore, the presence of a putative binding site within a promoter does not necessarily indicate that the factor will bind to the site in vivo. 2) Analysis of the binding affinity for a particular factor to a binding site in comparison to other related factors, via in vitro competition assays and quantitative titrations. This will provide information on how strongly these factors are binding to the sites, but without knowledge of all the factors present in a single cell it is difficult to recreate the in vivo conditions. 3) Generation of transgenic plants or microinjection of DNA/RNA to express a particular factor ectopically, reduce expression of the factor via **antisense**

expression, and creation of dominant negative mutants by overexpression of key dimerization domains may provide information concerning what biological pathways these factors influence. 4) Isolation of mutations in particular transcription factors has been extremely informative in floral development. However, this approach usually entails isolation of a mutant due to a **phenotype** and eventual mutated locus. The cloning of the locus may or may not involve a transcription factor. 5) Many plant transcription factors have been isolated via sequence similarity to other previously identified and/or characterized transcription factors. However, the biological role of many of these factors is not known. In addition to ectopic expression of these factors by creating transgenic plants, isolation of a **loss-of-function** mutation may provide valuable information concerning the role of this factor in vivo. Many **loss-of-function** mutations in MADS box genes have led to a better understanding of how the MADS domain proteins interact with one another as well as how they influence floral development. (ABSTRACT TRUNCATED)